SEQUENCE LISTING

<110> Glucksmann, Maria Alexandra
Silos-Santiago, Inmaculada

<120> Novel Seven-Transmembrane
Proteins/G-Protein Coupled Receptors

<130> 35800/208932

<150> 60/182,061
<151> 2000-02-11

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agtttgcaag gagtgagatt acagtggcct gcacctggct tattttggta ttttaagtaa     180
agacagggtt tcaccatgtt ggccaggctg ttcttgaact cctgacctca agtgttcccc     240
ntgcctcggg cctcccaaag tgctgggatt acaggcatga accaccatcc ccagccttct     300
ctcttcttaa taatggcttt ct atg tct ttc act tct ctc ata ccc tca ctc      352
                         Met Ser Phe Thr Ser Leu Ile Pro Ser Leu
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tgt ttc tcc ttg act ctc cca ttc ctg ttt tgt tat ctt tct tta tgg      400
Cys Phe Ser Leu Thr Leu Pro Phe Leu Phe Cys Tyr Leu Ser Leu Trp
                 15                  20                  25

ccg ttt ctt tct gct ttt ctg ttt atc act cgc tgg cta ctt gcc ttt      448
Pro Phe Leu Ser Ala Phe Leu Phe Ile Thr Arg Trp Leu Leu Ala Phe
             30                  35                  40

ctc tct cta ttc tct gtc tct gtc cct gtt tct tct gtt tca agt tca      496
Leu Ser Leu Phe Ser Val Ser Val Pro Val Ser Ser Val Ser Ser Ser
         45                  50                  55

atg gtt ctc tgt ctc tat ctc tct gtt tct gcc tct ccg tct gtc ttt      544
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Met Val Leu Cys Leu Tyr Leu Ser Val Ser Ala Ser Pro Ser Val Phe
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tgt ttc tct tgc atg cag ggc ccc ata ctg tgg atc atg gca aat ctg      592
Cys Phe Ser Cys Met Gln Gly Pro Ile Leu Trp Ile Met Ala Asn Leu
 75                  80                  85                  90

agc cag ccc tcc gaa ttt gtc ctc ttg ggc ttc tcc tcc ttt ggt gag      640
Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser Ser Phe Gly Glu
                 95                 100                 105

ctg cag gcc ctt ctg tat ggc ccc ttc ctc atg ctt tat ctt ctc gcc      688
Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu Tyr Leu Leu Ala
            110                 115                 120

ttc atg gga aac acc atc atc ata gtt atg gtc ata gct gac acc cac      736
Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile Ala Asp Thr His
        125                 130                 135

cta cat aca ccc atg tac ttc ttc ctg ggc aat ttt tcc ctg ctg gag      784
Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu
    140                 145                 150

atc ttg gta acc atg act gca gtg ccc agg atg ctc tca gac ctg ttg      832
Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu
155                 160                 165                 170

gtc ccc cac aaa gtc att acc ttc act ggc tgc atg gtc cag ttc tac      880
Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln Phe Tyr
                175                 180                 185

ttc cac ttt tcc ctg ggg tcc acc tcc ttc ctc atc ctg aca gac atg      928
Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met
            190                 195                 200

gcc ctt gat cgc ttt gtg gcc atc tgc cac cca ctg cgc tat ggc act      976
Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr
        205                 210                 215

ctg atg agc cgg gct atg tgt gtc cag ctg gct ggg gct gcc tgg gca     1024
Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala
    220                 225                 230

gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt     1072
Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu
235                 240                 245                 250

gat tac tgc cat ggc ggc gtc atc aac cac ttc ttc tgt gac aat gaa     1120
Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu
                255                 260                 265

cct ctc ctg cag ttg tca tgc tct gac act cgc ctg ttg gaa ttc tgg     1168
Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp
            270                 275                 280
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Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr
        285                 290                 295

ctc atc tcc tat ggc tac ata gtg acc act gtg ctg cgg atc ccc tct     1264
Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile Pro Ser
    300                 305                 310

gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca     1312
Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr
315                 320                 325                 330

ctg gtc ttc atc ggc tac agt agt acc atc ttt ctg tat gtc agg cct     1360
Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro
                335                 340                 345

ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act     1408
Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr
            350                 355                 360

tca gtt ctc acc ccc ttt ctc aat ccc ttt atc ctt acc ttc tgc aat     1456
Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu Thr Phe Cys Asn
        365                 370                 375

cag aca gtt aaa aca gtg cta cag ggg cag atg cag agg ctg aaa ggc     1504
Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln Arg Leu Lys Gly
    380                 385                 390

ctt tgc aag gca caa tga tgagcccagg gcccagggga acctggcctg            1552
Leu Cys Lys Ala Gln  *
395

cctccattga gcagttctgt ggggagggag acctccagca agtgggaaga acactgctga   1612
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ctggcccaaa gctcttatgg accaccatgg aagagttccc tacatcccct ggcagccgta   1732
agaactctga gagtagccca gagctttcag taaagggaag tgcatgtgct ttgcatttaa   1792
ggaagagcag ccmagaagtg ctctatgatc aagaggtagt cgacgcggcc gcgtcgacgg   1852
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            20                  25                  30
Leu Phe Ile Thr Arg Trp Leu Leu Ala Phe Leu Ser Leu Phe Ser Val
        35                  40                  45
Ser Val Pro Val Ser Ser Val Ser Ser Ser Met Val Leu Cys Leu Tyr
    50                  55                  60
Leu Ser Val Ser Ala Ser Pro Ser Val Phe Cys Phe Ser Cys Met Gln
65                  70                  75                  80
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Gly Pro Ile Leu Trp Ile Met Ala Asn Leu Ser Gln Pro Ser Glu Phe
                85                  90                  95
Val Leu Leu Gly Phe Ser Ser Phe Gly Glu Leu Gln Ala Leu Leu Tyr
            100                 105                 110
Gly Pro Phe Leu Met Leu Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile
        115                 120                 125
Ile Ile Val Met Val Ile Ala Asp Thr His Leu His Thr Pro Met Tyr
    130                 135                 140
Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu Ile Leu Val Thr Met Thr
145                 150                 155                 160
Ala Val Pro Arg Met Leu Ser Asp Leu Leu Val Pro His Lys Val Ile
                165                 170                 175
Thr Phe Thr Gly Cys Met Val Gln Phe Tyr Phe His Phe Ser Leu Gly
            180                 185                 190
Ser Thr Ser Phe Leu Ile Leu Thr Asp Met Ala Leu Asp Arg Phe Val
        195                 200                 205
Ala Ile Cys His Pro Leu Arg Tyr Gly Thr Leu Met Ser Arg Ala Met
    210                 215                 220
Cys Val Gln Leu Ala Gly Ala Ala Trp Ala Ala Pro Phe Leu Ala Met
225                 230                 235                 240
Val Pro Thr Val Leu Ser Arg Ala His Leu Asp Tyr Cys His Gly Gly
                245                 250                 255
Val Ile Asn His Phe Phe Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser
            260                 265                 270
Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp Asp Phe Leu Met Ala Leu
        275                 280                 285
Thr Phe Val Leu Ser Ser Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr
    290                 295                 300
Ile Val Thr Thr Val Leu Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys
305                 310                 315                 320
Ala Phe Ser Thr Cys Gly Ser His Leu Thr Leu Val Phe Ile Gly Tyr
                325                 330                 335
Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro Gly Lys Ala His Ser Val
            340                 345                 350
Gln Val Arg Lys Val Val Ala Leu Val Thr Ser Val Leu Thr Pro Phe
        355                 360                 365
Leu Asn Pro Phe Ile Leu Thr Phe Cys Asn Gln Thr Val Lys Thr Val
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gcctttctct ctctattctc tgtctctgtc cctgtttctt ctgtttcaag ttcaatggtt     180
ctctgtctct atctctctgt ttctgcctct ccgtctgtct tttgtttctc ttgcatgcag     240
ggccccatac tgtggatcat ggcaaatctg agccagccct ccgaatttgt cctcttgggc     300
ttctcctcct ttggtgagct gcaggccctt ctgtatggcc ccttcctcat gctttatctt     360
ctcgccttca tgggaaacac catcatcata gttatggtca tagctgacac ccacctacat     420
acacccatgt acttcttcct gggcaatttt tccctgctgg agatcttggt aaccatgact     480
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gcagtgccca ggatgctctc agacctgttg gtcccccaca aagtcattac cttcactggc     540
tgcatggtcc agttctactt ccacttttcc ctggggtcca cctccttcct catcctgaca     600
gacatggccc ttgatcgctt tgtggccatc tgccacccac tgcgctatgg cactctgatg     660
agccgggcta tgtgtgtcca gctggctggg gctgcctggg cagctccttt cctagccatg     720
gtacccactg tcctctcccg agctcatctt gattactgcc atggcggcgt catcaaccac     780
ttcttctgtg acaatgaacc tctcctgcag ttgtcatgct ctgacactcg cctgttggaa     840
ttctgggact ttctgatggc cttgaccttt gtcctcagct ccttcctggt gaccctcatc     900
tcctatggct acatagtgac cactgtgctg cggatcccct ctgccagcag ctgccagaag     960
gctttctcca cttgcgggtc tcacctcaca ctggtcttca tcggctacag tagtaccatc    1020
tttctgtatg tcaggcctgg caaagctcac tctgtgcaag tcaggaaggt cgtggccttg    1080
gtgacttcag ttctcacccc ctttctcaat ccctttatcc ttaccttctg caatcagaca    1140
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ctgcctccgc ctccccagaa gcaacatccg aggctcggcg cagaagagcc gccgctgtga     180
gccgtgccgt accggccccc gccgccgccc gaggagaacg ggagggcggg cgagagagcc     240
ggggagttgc ggagcccgcc cgccggcagc gccgctcccc agggagggag tccgcagcct     300
gaggtcttct ccaagaaaaa aaaaaagaaa aaaaaaaaca ac atg gct gca aag         354
                                                Met Ala Ala Lys
                                                 1

gag aaa ctg gag gca gtg tta aat gtg gcc ctg agg gtg cca agc atc       402
Glu Lys Leu Glu Ala Val Leu Asn Val Ala Leu Arg Val Pro Ser Ile
 5                  10                  15                  20

atg ctg ttg gat gtc ctg tac aga tgg gat gtc agc tcc ttt ttc cag       450
Met Leu Leu Asp Val Leu Tyr Arg Trp Asp Val Ser Ser Phe Phe Gln
                25                  30                  35

cag atc caa aga agt agc ctt agt aat aac cct ctt ttc cag tat aag       498
Gln Ile Gln Arg Ser Ser Leu Ser Asn Asn Pro Leu Phe Gln Tyr Lys
            40                  45                  50

tat ttg gct ctt aat atg cat tat gta ggt tat atc tta agt gtg gtg       546
Tyr Leu Ala Leu Asn Met His Tyr Val Gly Tyr Ile Leu Ser Val Val
        55                  60                  65

ctg cta aca ttg ccc agg cag cat ctg gtt cag ctt tat cta tat ttt       594
Leu Leu Thr Leu Pro Arg Gln His Leu Val Gln Leu Tyr Leu Tyr Phe
    70                  75                  80

ttg act gct ctg ctc ctc tat gct gga cat caa att tcc agg gac tat       642
Leu Thr Ala Leu Leu Leu Tyr Ala Gly His Gln Ile Ser Arg Asp Tyr
 85                  90                  95                 100
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gtt cgg agt gaa ctg gag ttt gcc tat gag gga cca atg tat tta gaa      690
Val Arg Ser Glu Leu Glu Phe Ala Tyr Glu Gly Pro Met Tyr Leu Glu
                105                 110                 115

cct ctc tct atg aat cgg ttt acc aca gcc tta ata ggt cag ttg gtg      738
Pro Leu Ser Met Asn Arg Phe Thr Thr Ala Leu Ile Gly Gln Leu Val
            120                 125                 130

gtg tgt act tta tgc tcc tgt gtc atg aaa aca aag cag att tgg ctg      786
Val Cys Thr Leu Cys Ser Cys Val Met Lys Thr Lys Gln Ile Trp Leu
        135                 140                 145

ttt tca gct cac atg ctt cct ctg cta gca cga ctc tgc ctt gtt cct      834
Phe Ser Ala His Met Leu Pro Leu Leu Ala Arg Leu Cys Leu Val Pro
    150                 155                 160

ttg gag aca att gtt atc atc aat aaa ttt gct atg att ttt act gga      882
Leu Glu Thr Ile Val Ile Ile Asn Lys Phe Ala Met Ile Phe Thr Gly
165                 170                 175                 180

ttg gaa gtt ctc tat ttt ctt ggg tct aat ctt ttg gta cct tat aac      930
Leu Glu Val Leu Tyr Phe Leu Gly Ser Asn Leu Leu Val Pro Tyr Asn
                185                 190                 195

ctt gct aaa tct gca tac aga gaa ttg gtt cag gta gtg gag gta tat      978
Leu Ala Lys Ser Ala Tyr Arg Glu Leu Val Gln Val Val Glu Val Tyr
            200                 205                 210

ggc ctt ctc gcc ttg gga atg tcc ctg tgg aat caa ctg gta gtc cct     1026
Gly Leu Leu Ala Leu Gly Met Ser Leu Trp Asn Gln Leu Val Val Pro
        215                 220                 225

gtt ctt ttc atg gtt ttc tgg ctc gtc tta ttt gct ctt cag att tac     1074
Val Leu Phe Met Val Phe Trp Leu Val Leu Phe Ala Leu Gln Ile Tyr
    230                 235                 240

tcc tat ttc agt act cga gat cag cct gca tca cgt gag agg ctt ctt     1122
Ser Tyr Phe Ser Thr Arg Asp Gln Pro Ala Ser Arg Glu Arg Leu Leu
245                 250                 255                 260

ttc ctt ttt ctg aca agt att gcg gaa tgc tgc agc act cct tac tct     1170
Phe Leu Phe Leu Thr Ser Ile Ala Glu Cys Cys Ser Thr Pro Tyr Ser
                265                 270                 275

ctt ttg ggt ttg gtc ttc acg gtt tct ttt gtt gcc ttg ggt gtt ctc     1218
Leu Leu Gly Leu Val Phe Thr Val Ser Phe Val Ala Leu Gly Val Leu
            280                 285                 290

aca ctc tgc aag ttt tac ttg cag ggt tat cga gct ttc atg aat gat     1266
Thr Leu Cys Lys Phe Tyr Leu Gln Gly Tyr Arg Ala Phe Met Asn Asp
        295                 300                 305

cct gcc atg aat cgg ggc atg aca gaa gga gta acg ctg tta atc ctg     1314
Pro Ala Met Asn Arg Gly Met Thr Glu Gly Val Thr Leu Leu Ile Leu
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    310                 315                 320

gca gtg cag act ggg ctg ata gaa ctg cag gtt gtt cat cgg gca ttc     1362
Ala Val Gln Thr Gly Leu Ile Glu Leu Gln Val Val His Arg Ala Phe
325                 330                 335                 340

ttg ctc agt att atc ctt ttc att gtc gta gct tct atc cta cag tct     1410
Leu Leu Ser Ile Ile Leu Phe Ile Val Val Ala Ser Ile Leu Gln Ser
                345                 350                 355

atg tta gaa att gca gat cct att gtt ttg gca ctg gga gca tct aga     1458
Met Leu Glu Ile Ala Asp Pro Ile Val Leu Ala Leu Gly Ala Ser Arg
            360                 365                 370

gac aag agc ttg tgg aaa cac ttc cgt gct gta agc ctt tgt tta ttt     1506
Asp Lys Ser Leu Trp Lys His Phe Arg Ala Val Ser Leu Cys Leu Phe
        375                 380                 385

tta ttg gta ttc cct gct tat atg gct tat atg att tgc cag ttt ttc     1554
Leu Leu Val Phe Pro Ala Tyr Met Ala Tyr Met Ile Cys Gln Phe Phe
    390                 395                 400

cac atg gat ttt tgg ctt ctt atc att att tcc agc agc att ctt acc     1602
His Met Asp Phe Trp Leu Leu Ile Ile Ile Ser Ser Ser Ile Leu Thr
405                 410                 415                 420

tct ctt cag gtt ctg gga aca ctt ttt att tat gtc tta ttt atg gtt     1650
Ser Leu Gln Val Leu Gly Thr Leu Phe Ile Tyr Val Leu Phe Met Val
                425                 430                 435

gag gaa ttc aga aaa gag cca gtg gaa aac atg gat gat gtc atc tac     1698
Glu Glu Phe Arg Lys Glu Pro Val Glu Asn Met Asp Asp Val Ile Tyr
            440                 445                 450

tat gtg aat ggc act tac cgc ctg ctg gag ttt ctt gtg gcc ctc tgt     1746
Tyr Val Asn Gly Thr Tyr Arg Leu Leu Glu Phe Leu Val Ala Leu Cys
        455                 460                 465

gtg gtg gcc tat ggc gtc tca gag acc atc ttt gga gaa tgg aca gtg     1794
Val Val Ala Tyr Gly Val Ser Glu Thr Ile Phe Gly Glu Trp Thr Val
    470                 475                 480

atg ggc tca atg atc atc ttc att cat tcc tac tat aac gtg tgg ctt     1842
Met Gly Ser Met Ile Ile Phe Ile His Ser Tyr Tyr Asn Val Trp Leu
485                 490                 495                 500

cgg gcc cag ctg ggg tgg aag agc ttt ctt ctc cgc agg gat gct gtg     1890
Arg Ala Gln Leu Gly Trp Lys Ser Phe Leu Leu Arg Arg Asp Ala Val
                505                 510                 515

aat aag att aaa tcg tta ccc att gct acg aaa gag cag ctt gag aaa     1938
Asn Lys Ile Lys Ser Leu Pro Ile Ala Thr Lys Glu Gln Leu Glu Lys
            520                 525                 530

cac aat gat att tgt gcc atc tgt tat cag gac atg aaa tct gct gtg     1986
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His Asn Asp Ile Cys Ala Ile Cys Tyr Gln Asp Met Lys Ser Ala Val
535 540 545

atc acg cct tgc agt cat ttt ttc cat gca ggc tgt ctt aag aaa tgg 2034
Ile Thr Pro Cys Ser His Phe Phe His Ala Gly Cys Leu Lys Lys Trp
550 555 560

ctg tat gtc cag gag acc tgc cct ctg tgc cac tgc cat ctg aaa aac 2082
Leu Tyr Val Gln Glu Thr Cys Pro Leu Cys His Cys His Leu Lys Asn
565 570 575 580

tcc tcc cag ctt cca gga tta gga act gag cca gtt cta cag cct cat 2130
Ser Ser Gln Leu Pro Gly Leu Gly Thr Glu Pro Val Leu Gln Pro His
585 590 595

gct gga gct gag caa aac gtc atg ttt cag gaa ggt act gaa ccc cca 2178
Ala Gly Ala Glu Gln Asn Val Met Phe Gln Glu Gly Thr Glu Pro Pro
600 605 610

ggc cag gag cat act cca ggg acc agg ata cag gaa ggt tcc agg gac 2226
Gly Gln Glu His Thr Pro Gly Thr Arg Ile Gln Glu Gly Ser Arg Asp
615 620 625

aat aat gag tac att gcc aga cga cca gat aac cag gaa ggg gct ttt 2274
Asn Asn Glu Tyr Ile Ala Arg Arg Pro Asp Asn Gln Glu Gly Ala Phe
630 635 640

gac ccc aaa gaa tat cct cac agt gcg aaa gat gaa gca cat cct gtt 2322
Asp Pro Lys Glu Tyr Pro His Ser Ala Lys Asp Glu Ala His Pro Val
645 650 655 660

gaa tca gcc tag aggagaagca gcaggaatga tgctttgata ctctggagga 2374
Glu Ser Ala *

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35 40 45
Phe Gln Tyr Lys Tyr Leu Ala Leu Asn Met His Tyr Val Gly Tyr Ile
50 55 60
Leu Ser Val Val Leu Leu Thr Leu Pro Arg Gln His Leu Val Gln Leu
65 70 75 80
Tyr Leu Tyr Phe Leu Thr Ala Leu Leu Leu Tyr Ala Gly His Gln Ile
85 90 95
Ser Arg Asp Tyr Val Arg Ser Glu Leu Glu Phe Ala Tyr Glu Gly Pro
100 105 110
Met Tyr Leu Glu Pro Leu Ser Met Asn Arg Phe Thr Thr Ala Leu Ile
115 120 125
Gly Gln Leu Val Val Cys Thr Leu Cys Ser Cys Val Met Lys Thr Lys
130 135 140
Gln Ile Trp Leu Phe Ser Ala His Met Leu Pro Leu Leu Ala Arg Leu
145 150 155 160
Cys Leu Val Pro Leu Glu Thr Ile Val Ile Ile Asn Lys Phe Ala Met
165 170 175
Ile Phe Thr Gly Leu Glu Val Leu Tyr Phe Leu Gly Ser Asn Leu Leu
180 185 190
Val Pro Tyr Asn Leu Ala Lys Ser Ala Tyr Arg Glu Leu Val Gln Val
195 200 205
Val Glu Val Tyr Gly Leu Leu Ala Leu Gly Met Ser Leu Trp Asn Gln
210 215 220
Leu Val Val Pro Val Leu Phe Met Val Phe Trp Leu Val Leu Phe Ala
225 230 235 240
Leu Gln Ile Tyr Ser Tyr Phe Ser Thr Arg Asp Gln Pro Ala Ser Arg
245 250 255
Glu Arg Leu Leu Phe Leu Phe Leu Thr Ser Ile Ala Glu Cys Cys Ser
260 265 270
Thr Pro Tyr Ser Leu Leu Gly Leu Val Phe Thr Val Ser Phe Val Ala
275 280 285
Leu Gly Val Leu Thr Leu Cys Lys Phe Tyr Leu Gln Gly Tyr Arg Ala
290 295 300
Phe Met Asn Asp Pro Ala Met Asn Arg Gly Met Thr Glu Gly Val Thr
305 310 315 320
Leu Leu Ile Leu Ala Val Gln Thr Gly Leu Ile Glu Leu Gln Val Val
325 330 335
His Arg Ala Phe Leu Leu Ser Ile Ile Leu Phe Ile Val Val Ala Ser
340 345 350
Ile Leu Gln Ser Met Leu Glu Ile Ala Asp Pro Ile Val Leu Ala Leu
355 360 365
Gly Ala Ser Arg Asp Lys Ser Leu Trp Lys His Phe Arg Ala Val Ser

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    370                 375                 380
Leu Cys Leu Phe Leu Leu Val Phe Pro Ala Tyr Met Ala Tyr Met Ile
385                 390                 395                 400
Cys Gln Phe Phe His Met Asp Phe Trp Leu Leu Ile Ile Ile Ser Ser
                405                 410                 415
Ser Ile Leu Thr Ser Leu Gln Val Leu Gly Thr Leu Phe Ile Tyr Val
            420                 425                 430
Leu Phe Met Val Glu Glu Phe Arg Lys Glu Pro Val Glu Asn Met Asp
        435                 440                 445
Asp Val Ile Tyr Tyr Val Asn Gly Thr Tyr Arg Leu Leu Glu Phe Leu
    450                 455                 460
Val Ala Leu Cys Val Val Ala Tyr Gly Val Ser Glu Thr Ile Phe Gly
465                 470                 475                 480
Glu Trp Thr Val Met Gly Ser Met Ile Ile Phe Ile His Ser Tyr Tyr
                485                 490                 495
Asn Val Trp Leu Arg Ala Gln Leu Gly Trp Lys Ser Phe Leu Leu Arg
            500                 505                 510
Arg Asp Ala Val Asn Lys Ile Lys Ser Leu Pro Ile Ala Thr Lys Glu
        515                 520                 525
Gln Leu Glu Lys His Asn Asp Ile Cys Ala Ile Cys Tyr Gln Asp Met
    530                 535                 540
Lys Ser Ala Val Ile Thr Pro Cys Ser His Phe Phe His Ala Gly Cys
545                 550                 555                 560
Leu Lys Lys Trp Leu Tyr Val Gln Glu Thr Cys Pro Leu Cys His Cys
                565                 570                 575
His Leu Lys Asn Ser Ser Gln Leu Pro Gly Leu Gly Thr Glu Pro Val
            580                 585                 590
Leu Gln Pro His Ala Gly Ala Glu Gln Asn Val Met Phe Gln Glu Gly
        595                 600                 605
Thr Glu Pro Pro Gly Gln Glu His Thr Pro Gly Thr Arg Ile Gln Glu
    610                 615                 620
Gly Ser Arg Asp Asn Asn Glu Tyr Ile Ala Arg Arg Pro Asp Asn Gln
625                 630                 635                 640
Glu Gly Ala Phe Asp Pro Lys Glu Tyr Pro His Ser Ala Lys Asp Glu
                645                 650                 655
Ala His Pro Val Glu Ser Ala
            660
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<210> 6
<211> 1992
<212> DNA
<213> Homo sapiens

<400> 6

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atgctgttgg atgtcctgta cagatgggat gtcagctcct ttttccagca gatccaaaga     120
agtagcctta gtaataaccc tcttttccag tataagtatt tggctcttaa tatgcattat     180
gtaggttata tcttaagtgt ggtgctgcta acattgccca ggcagcatct ggttcagctt     240
tatctatatt ttttgactgc tctgctcctc tatgctggac atcaaatttc cagggactat     300
gttcggagtg aactggagtt tgcctatgag ggaccaatgt atttagaacc tctctctatg     360
aatcggttta ccacagcctt aataggtcag ttggtggtgt gtactttatg ctcctgtgtc     420
atgaaaacaa agcagatttg gctgttttca gctcacatgc ttcctctgct agcacgactc     480
tgccttgttc ctttggagac aattgttatc atcaataaat ttgctatgat ttttactgga     540
ttggaagttc tctatttttct tgggtctaat cttttggtac cttataacct tgctaaatct     600
gcatacagag aattggttca ggtagtggag gtatatggcc ttctcgcctt gggaatgtcc     660
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ctgtggaatc aactggtagt ccctgttctt ttcatggttt tctggctcgt cttatttgct     720
cttcagattt actcctattt cagtactcga gatcagcctg catcacgtga gaggcttctt     780
ttccttttc tgacaagtat tgcggaatgc tgcagcactc cttactctct tttgggtttg      840
gtcttcacgg tttcttttgt tgccttgggt gttctcacac tctgcaagtt ttacttgcag     900
ggttatcgag ctttcatgaa tgatcctgcc atgaatcggg gcatgacaga aggagtaacg     960
ctgttaatcc tggcagtgca gactgggctg atagaactgc aggttgttca tcgggcattc    1020
ttgctcagta ttatcctttt cattgtcgta gcttctatcc tacagtctat gttagaaatt    1080
gcagatccta ttgttttggc actgggagca tctagagaca agagcttgtg gaaacacttc    1140
cgtgctgtaa gcctttgttt atttttattg gtattccctg cttatatggc ttatatgatt    1200
tgccagtttt tccacatgga tttttggctt cttatcatta tttccagcag cattcttacc    1260
tctcttcagg ttctgggaac acttttttatt tatgtcttat ttatggttga ggaattcaga    1320
aaagagccag tggaaaacat ggatgatgtc atctactatg tgaatggcac ttaccgcctg    1380
ctggagtttc ttgtggccct ctgtgtggtg gcctatggcg tctcagagac catctttgga    1440
gaatggacag tgatgggctc aatgatcatc ttcattcatt cctactataa cgtgtggctt    1500
cgggcccagc tggggtggaa gagctttctt ctccgcaggg atgctgtgaa taagattaaa    1560
tcgttaccca ttgctacgaa agagcagctt gagaaacaca atgatatttg tgccatctgt    1620
tatcaggaca tgaaatctgc tgtgatcacg ccttgcagtc atttttcca tgcaggctgt     1680
cttaagaaat ggctgtatgt ccaggagacc tgccctctgt gccactgcca tctgaaaaac    1740
tcctcccagc ttccaggatt aggaactgag ccagttctac agcctcatgc tggagctgag    1800
caaaacgtca tgtttcagga aggtactgaa cccccaggcc aggagcatac tccagggacc    1860
aggatacagg aaggttccag ggacaataat gagtacattg ccagacgacc agataaccag    1920
gaaggggctt ttgaccccaa agaatatcct cacagtgcga aagatgaagc acatcctgtt    1980
gaatcagcct ag                                                       1992

<210> 7
<211> 1587
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (309)...(1427)

<400> 7
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gtggtccctg ccccacccgc gcggagccag agaggaggcg gttgtcaagg cgacgtgggt     120
aggaggagag gacagaggga ggaggaagga tgggcggtgt tggcgtagcc gcagggaggt     180
gactgaagca gcctggcctc ttgcatcctc cgcctgtgta cctccctccc ctttttttcc     240
gccttctgcc agcagaagca gcagccgcag cacctgagcc gctactgccg ctcactcagg     300
acaacgct atg gct gag cct ggg cac agc cac cat ctc tcc gcc aga gtc       350
         Met Ala Glu Pro Gly His Ser His His Leu Ser Ala Arg Val
          1               5                  10

agg gga aga act gag agg cgc ata ccc cgg ctg tgg cgg ctg ctg ctc       398
Arg Gly Arg Thr Glu Arg Arg Ile Pro Arg Leu Trp Arg Leu Leu Leu
 15                  20                  25                  30

tgg gct ggg acc gcc ttc cag gtg acc cag gga acg gga ccg gag ctt       446
Trp Ala Gly Thr Ala Phe Gln Val Thr Gln Gly Thr Gly Pro Glu Leu
                 35                  40                  45

cac gcc tgc aaa gag tct gag tac cac tat gag tac acg gcg tgt gac       494
His Ala Cys Lys Glu Ser Glu Tyr His Tyr Glu Tyr Thr Ala Cys Asp
             50                  55                  60
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agc acg ggt tcc agg tgg agg gtc gcc gtg ccg cat acc ccg ggc ctg      542
Ser Thr Gly Ser Arg Trp Arg Val Ala Val Pro His Thr Pro Gly Leu
         65                  70                  75

tgc acc agc ctg cct gac ccc gtc aag ggc acc gag tgc tcc ttc tcc      590
Cys Thr Ser Leu Pro Asp Pro Val Lys Gly Thr Glu Cys Ser Phe Ser
     80                  85                  90

tgc aac gcc ggg gag ttt ctg gat atg aag gac cag tca tgt aag cca      638
Cys Asn Ala Gly Glu Phe Leu Asp Met Lys Asp Gln Ser Cys Lys Pro
 95                 100                 105                 110

tgc gct gag ggc cgc tac tcc ctc ggc aca ggc att cgg ttt gat gag      686
Cys Ala Glu Gly Arg Tyr Ser Leu Gly Thr Gly Ile Arg Phe Asp Glu
                115                 120                 125

tgg gat gag ctg ccc cat ggc ttt gcc agc ctc tca gcc aac atg gag      734
Trp Asp Glu Leu Pro His Gly Phe Ala Ser Leu Ser Ala Asn Met Glu
            130                 135                 140

ctg gat gac agt gct gct gag tcc acc ggg aac tgt act tcg tcc aag      782
Leu Asp Asp Ser Ala Ala Glu Ser Thr Gly Asn Cys Thr Ser Ser Lys
        145                 150                 155

tgg gtt ccc cgg ggc gac tac atc gcc tcc aac acg gac gaa tgc aca      830
Trp Val Pro Arg Gly Asp Tyr Ile Ala Ser Asn Thr Asp Glu Cys Thr
    160                 165                 170

gcc aca ctg atg tac gcc gtc aac ctg aag caa tct ggc acc gtt aac      878
Ala Thr Leu Met Tyr Ala Val Asn Leu Lys Gln Ser Gly Thr Val Asn
175                 180                 185                 190

ttc gaa tac tac tat cca gac tcc agc atc atc ttt gag ttt ttc gtt      926
Phe Glu Tyr Tyr Tyr Pro Asp Ser Ser Ile Ile Phe Glu Phe Phe Val
                195                 200                 205

cag aat gac cag tgc cag ccc aat gca gat gac tcc agg tgg atg aag      974
Gln Asn Asp Gln Cys Gln Pro Asn Ala Asp Asp Ser Arg Trp Met Lys
            210                 215                 220

acc aca gag aaa gga tgg gaa ttc cac agt gtg gag cta aat cga ggc     1022
Thr Thr Glu Lys Gly Trp Glu Phe His Ser Val Glu Leu Asn Arg Gly
        225                 230                 235

aat aat gtc ctc tat tgg aga acc aca gcc ttc tca gta tgg acc aaa     1070
Asn Asn Val Leu Tyr Trp Arg Thr Thr Ala Phe Ser Val Trp Thr Lys
    240                 245                 250

gta ccc aag cct gtg ctg gtg aga aac att gcc ata aca ggg gtg gcc     1118
Val Pro Lys Pro Val Leu Val Arg Asn Ile Ala Ile Thr Gly Val Ala
255                 260                 265                 270

tac act tca gaa tgc ttc ccc tgc aaa cct ggc acg tat gca gac aag     1166
Tyr Thr Ser Glu Cys Phe Pro Cys Lys Pro Gly Thr Tyr Ala Asp Lys
                275                 280                 285
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cag ggc tcc tct ttc tgc aaa ctt tgc cca gcc aac tct tat tca aat     1214
Gln Gly Ser Ser Phe Cys Lys Leu Cys Pro Ala Asn Ser Tyr Ser Asn
            290                 295                 300

aaa gga gaa act tct tgc cac cag tgt gac cct gac aaa tac tca ggt     1262
Lys Gly Glu Thr Ser Cys His Gln Cys Asp Pro Asp Lys Tyr Ser Gly
        305                 310                 315

gat gtt tct gag ggt ggg aag agt ttg ggg ata gag agt acc acc aaa     1310
Asp Val Ser Glu Gly Gly Lys Ser Leu Gly Ile Glu Ser Thr Thr Lys
    320                 325                 330

aca cac aag gag ata cca ggg aat aga gcc atc ctt ctg gcc aag ctg     1358
Thr His Lys Glu Ile Pro Gly Asn Arg Ala Ile Leu Leu Ala Lys Leu
335                 340                 345                 350

agg atg gta att ctt aaa ccc ttc ctt tct gga tcc tgg aat acc ctt     1406
Arg Met Val Ile Leu Lys Pro Phe Leu Ser Gly Ser Trp Asn Thr Leu
                355                 360                 365

gcc aat cca tat atc cat taa tcactttgtc attttttttt ttttttgaaa        1457
Ala Asn Pro Tyr Ile His  *
            370

aagggtctcg ctttgtcacc caggctgagg tgccgtggtg cgatcatggc tcactgcagc   1517
ctcaaactcc ctgtctctca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   1577
aaaagggcgg                                                          1587

<210> 8
<211> 372
<212> PRT
<213> Homo sapiens

<400> 8
Met Ala Glu Pro Gly His Ser His His Leu Ser Ala Arg Val Arg Gly
 1               5                  10                  15
Arg Thr Glu Arg Arg Ile Pro Arg Leu Trp Arg Leu Leu Leu Trp Ala
            20                  25                  30
Gly Thr Ala Phe Gln Val Thr Gln Gly Thr Gly Pro Glu Leu His Ala
        35                  40                  45
Cys Lys Glu Ser Glu Tyr His Tyr Glu Tyr Thr Ala Cys Asp Ser Thr
    50                  55                  60
Gly Ser Arg Trp Arg Val Ala Val Pro His Thr Pro Gly Leu Cys Thr
65                  70                  75                  80
Ser Leu Pro Asp Pro Val Lys Gly Thr Glu Cys Ser Phe Ser Cys Asn
                85                  90                  95
Ala Gly Glu Phe Leu Asp Met Lys Asp Gln Ser Cys Lys Pro Cys Ala
            100                 105                 110
Glu Gly Arg Tyr Ser Leu Gly Thr Gly Ile Arg Phe Asp Glu Trp Asp
        115                 120                 125
Glu Leu Pro His Gly Phe Ala Ser Leu Ser Ala Asn Met Glu Leu Asp
    130                 135                 140
Asp Ser Ala Ala Glu Ser Thr Gly Asn Cys Thr Ser Ser Lys Trp Val
145                 150                 155                 160
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Pro Arg Gly Asp Tyr Ile Ala Ser Asn Thr Asp Glu Cys Thr Ala Thr
                165                 170                 175
Leu Met Tyr Ala Val Asn Leu Lys Gln Ser Gly Thr Val Asn Phe Glu
            180                 185                 190
Tyr Tyr Tyr Pro Asp Ser Ser Ile Ile Phe Glu Phe Phe Val Gln Asn
        195                 200                 205
Asp Gln Cys Gln Pro Asn Ala Asp Asp Ser Arg Trp Met Lys Thr Thr
    210                 215                 220
Glu Lys Gly Trp Glu Phe His Ser Val Glu Leu Asn Arg Gly Asn Asn
225                 230                 235                 240
Val Leu Tyr Trp Arg Thr Thr Ala Phe Ser Val Trp Thr Lys Val Pro
                245                 250                 255
Lys Pro Val Leu Val Arg Asn Ile Ala Ile Thr Gly Val Ala Tyr Thr
            260                 265                 270
Ser Glu Cys Phe Pro Cys Lys Pro Gly Thr Tyr Ala Asp Lys Gln Gly
        275                 280                 285
Ser Ser Phe Cys Lys Leu Cys Pro Ala Asn Ser Tyr Ser Asn Lys Gly
    290                 295                 300
Glu Thr Ser Cys His Gln Cys Asp Pro Asp Lys Tyr Ser Gly Asp Val
305                 310                 315                 320
Ser Glu Gly Gly Lys Ser Leu Gly Ile Glu Ser Thr Thr Lys Thr His
                325                 330                 335
Lys Glu Ile Pro Gly Asn Arg Ala Ile Leu Leu Ala Lys Leu Arg Met
            340                 345                 350
Val Ile Leu Lys Pro Phe Leu Ser Gly Ser Trp Asn Thr Leu Ala Asn
        355                 360                 365
Pro Tyr Ile His
    370
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<210> 9
<211> 1119
<212> DNA
<213> Homo sapiens

<400> 9

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ggaacgggac cggagcttca cgcctgcaaa gagtctgagt accactatga gtacacggcg      180
tgtgacagca cgggttccag gtggagggtc gccgtgccgc ataccccggg cctgtgcacc      240
agcctgcctg accccgtcaa gggcaccgag tgctccttct cctgcaacgc cggggagttt      300
ctggatatga aggaccagtc atgtaagcca tgcgctgagg gccgctactc cctcggcaca      360
ggcattcggt ttgatgagtg ggatgagctg ccccatggct ttgccagcct ctcagccaac      420
atggagctgg atgacagtgc tgctgagtcc accgggaact gtacttcgtc caagtgggtt      480
ccccggggcg actacatcgc ctccaacacg gacgaatgca cagccacact gatgtacgcc      540
gtcaacctga agcaatctgg caccgttaac ttcgaatact actatccaga ctccagcatc      600
atctttgagt ttttcgttca gaatgaccag tgccagccca atgcagatga ctccaggtgg      660
atgaagacca cagagaaagg atgggaattc cacagtgtgg agctaaatcg aggcaataat      720
gtcctctatt ggagaaccac agccttctca gtatggacca aagtacccaa gcctgtgctg      780
gtgagaaaca ttgccataac aggggtggcc tacacttcag aatgcttccc ctgcaaacct      840
ggcacgtatg cagacaagca gggctcctct ttctgcaaac tttgcccagc caactcttat      900
tcaaataaag gagaaacttc ttgccaccag tgtgaccctg acaaatactc aggtgatgtt      960
tctgagggtg ggaagagttt ggggatagag agtaccacca aaacacacaa ggagatacca     1020
gggaatagag ccatccttct ggccaagctg aggatggtaa ttcttaaacc cttcctttct     1080
ggatcctgga ataccttgc caatccatat atccattaa                             1119
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<210> 10
<211> 259
<212> PRT
<213> Homo sapiens

<400> 10
Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
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Thr Pro Thr Asn Ile Phe Ile Leu Asn Leu Ala Val Ala Asp Leu Leu
            20   25   30
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
        35   40   45
Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
    50   55   60
Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile
65   70   75   80
Ser Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg
                85   90   95
Arg Arg Thr Ser Pro Arg Arg Ala Lys Val Val Ile Leu Leu Val Trp
            100   105   110
Val Leu Ala Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Val
        115   120   125
Lys Thr Val Glu Glu Gly Asn Gly Thr Leu Asn Val Asn Val Thr Val
    130   135   140
Cys Leu Ile Asp Phe Pro Glu Glu Ser Thr Ala Ser Val Ser Thr Trp
145   150   155   160
Leu Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu Pro
                165   170   175
Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg
            180   185   190
Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Val Phe Val Leu Cys
        195   200   205
Trp Leu Pro Tyr Phe Ile Val Leu Leu Leu Asp Thr Leu Cys Leu Ser
    210   215   220
Ile Ile Met Ser Ser Thr Cys Glu Leu Glu Arg Val Leu Pro Thr Ala
225   230   235   240
Leu Leu Val Thr Leu Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro
                245   250   255
Ile Ile Tyr